

Serial Number: 10/003608

ENTERED

#2

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were:
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited:
- ☒ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: deleted duplicate 42217-42237 responses

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

#2 OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/003,608

DATE: 12/17/2001
TIME: 20:15:46

Input Set : A:\PTO.AMC.TXT
Output Set: N:\CRF3\12172001\J003608.raw

PS

4 <110> APPLICANT: Bartha, Gabor
5 Walker, Michael
7 <120> TITLE OF INVENTION: METHODS FOR ANALYZING GENE EXPRESSION PATTERNS
10 <130> FILE REFERENCE: ICYTP012
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/003,608
C--> 12 <141> CURRENT FILING DATE: 2001-11-01
12 <150> PRIOR APPLICATION NUMBER: 60/245,081
13 <151> PRIOR FILING DATE: 2000-11-01
15 <160> NUMBER OF SEQ ID NOS: 30
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 4588
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
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27 tcctgccttg accaggactt gggactttgc gaaaggatcg cggggcccg agaggttaacc 180
28 gccgcgcctc ccggagaggt gttggagagc acaatggctg aacaagtcct tcctcaggct 240
29 ttgtatttga gcaatatgcg gaaagctgtg aagatacggg agagaactcc agaagacatt 300
30 tttaaaccta ctaatgggat cattcatcat tttaaaacca tgcaccgata cacactggaa 360
31 atgttcagaa cttgccagtt ttgtcctcag ttccgggaga tcatccacaa agccctcatc 420
32 gacagaaaca tccagggcac cctggaaagc cagaagaaac tcaactggtg tgcagaagtc 480
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37 aatcttatca aaatggcttc cacagacaca cccatggccc gaagtggact tcagtacaac 780
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40 ggtggaattt acttgccctc ccaactggcct gccaggaat gctacagata cccattgtt 960
41 ctcggtatg acagccatca ttttgtacct ttggtgacct tgaaggacag tgggcctgaa 1020
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44 atagaaatcc ccgtccaagg ctgggacctc ggcacaactc atctcatcaa tgccgcaaag 1200
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47 cagaatccca tggaaacctc cgtgccccag ctttctctca tggatgtaaa atgtgaaacg 1380
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55 aggacattta atgggatctg cagtacttgc ttcaaaagga ctacagcaga ggccctctcc 1860
56 agcctcagca ccagcctccc tcttctctgt caccagcgtt ccaagtcaga tccctcgcg 1920

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58 tgccgtgtctc aagctgcacg gactcctggg gacaggacgg ggacgagcaa gtgcagaaaa 2040
59 gccggctgcg tgtatttttg gactccagaa aacaagggtt ttgacacact gtgtttcatc 2100
60 gagtacagag aaaacaaaca ttttgctgct gcctcaggga aagtcagtcc cacagcgtcc 2160
61 aggttccaga acaccattcc gtgcctgggg agggaaatgc gcacccttgg aagcaccatg 2220
62 tttgaaggat actgccagaa gtgtttcatt gaagctcaga atcagagatt tcatgaggcc 2280
63 aaaaggacag aagagcaact gagatcgagc cagcgcagag atgtgcctcg aaccacacaa 2340
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67 tttggcaatg ccaagtgcaa cggtacttgc aacgaatgct ttcagttcaa gcagatgtat 2580
68 ggctaaccgg aaacagggtg gtcacctcct gcaagaagtg gggcctcgag ctgtcagtca 2640
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70 gagcaggaga ggaaagataa gctcttctg gtgcccacga tgctcaggtt tggtaaccgg 2760
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95 cttatggcct gaaaatattt gtgatccata actctacaca gcctttactc atactattag 4260
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97 caaagatacc aaataaactt cagtgttttc atctaattct cttaaagttg atatcttaat 4380
98 attttgtgtt gatcattatt tccattctta atgtgaaaaa aagtaattat ttatacttat 4440
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101 aaataaatta tttaaaaaaa aaaaaaaa 4588
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 790
105 <212> TYPE: PRT
106 <213> ORGANISM: Human

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111 Lys Ala Val Lys Ile Arg Glu Arg Thr Pro Glu Asp Ile Phe Lys Pro
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113 Thr Asn Gly Ile Ile His His Phe Lys Thr Met His Arg Tyr Thr Leu
114 35 40 45
115 Glu Met Phe Arg Thr Cys Gln Phe Cys Pro Gln Phe Arg Glu Ile Ile
116 50 55 60
117 His Lys Ala Leu Ile Asp Arg Asn Ile Gln Ala Thr Leu Glu Ser Gln
118 65 70 75 80
119 Lys Lys Leu Asn Trp Cys Arg Glu Val Arg Lys Leu Val Ala Leu Lys
120 85 90 95
121 Thr Asn Gly Asp Gly Asn Cys Leu Met His Ala Thr Ser Gln Tyr Met
122 100 105 110
123 Trp Gly Val Gln Asp Thr Asp Leu Val Leu Arg Lys Ala Leu Phe Ser
124 115 120 125
125 Thr Leu Lys Glu Thr Asp Thr Arg Asn Phe Lys Phe Arg Trp Gln Leu
126 130 135 140
127 Glu Ser Leu Lys Ser Gln Glu Phe Val Glu Thr Gly Leu Cys Tyr Asp
128 145 150 155 160
129 Thr Arg Asn Trp Asn Asp Glu Trp Asp Asn Leu Ile Lys Met Ala Ser
130 165 170 175
131 Thr Asp Thr Pro Met Ala Arg Ser Gly Leu Gln Tyr Asn Ser Leu Glu
132 180 185 190
133 Glu Ile His Ile Phe Val Leu Cys Asn Ile Leu Arg Arg Pro Ile Ile
134 195 200 205
135 Val Ile Ser Asp Lys Met Leu Arg Ser Leu Glu Ser Gly Ser Asn Phe
136 210 215 220
137 Ala Pro Leu Lys Val Gly Gly Ile Tyr Leu Pro Leu His Trp Pro Ala
138 225 230 235 240
139 Gln Glu Cys Tyr Arg Tyr Pro Ile Val Leu Gly Tyr Asp Ser His His
140 245 250 255
141 Phe Val Pro Leu Val Thr Leu Lys Asp Ser Gly Pro Glu Ile Arg Ala
142 260 265 270
143 Val Pro Leu Val Asn Arg Asp Arg Gly Arg Phe Glu Asp Leu Lys Val
144 275 280 285
145 His Phe Leu Thr Asp Pro Glu Asn Glu Met Lys Glu Lys Leu Leu Lys
146 290 295 300
147 Glu Tyr Leu Met Val Ile Glu Ile Pro Val Gln Gly Trp Asp His Gly
148 305 310 315 320
149 Thr Thr His Leu Ile Asn Ala Ala Lys Leu Asp Glu Ala Asn Leu Pro
150 325 330 335
151 Lys Glu Ile Asn Leu Val Asp Asp Tyr Phe Glu Leu Val Gln His Glu
152 340 345 350
153 Tyr Lys Lys Trp Gln Glu Asn Ser Glu Gln Gly Arg Arg Glu Gly His
154 355 360 365
155 Ala Gln Asn Pro Met Glu Pro Ser Val Pro Gln Leu Ser Leu Met Asp
156 370 375 380

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157 Val Lys Cys Glu Thr Pro Asn Cys Pro Phe Phe Met Ser Val Asn Thr
158 385 390 395 400
159 Gln Pro Leu Cys His Glu Cys Ser Glu Arg Arg Gln Lys Asn Gln Asn
160 405 410 415
161 Lys Leu Pro Lys Leu Asn Ser Lys Pro Gly Pro Glu Gly Leu Pro Gly
162 420 425 430
163 Met Ala Leu Gly Ala Ser Arg Gly Glu Ala Tyr Glu Pro Leu Ala Trp
164 435 440 445
165 Asn Pro Glu Glu Ser Thr Gly Gly Pro His Ser Ala Pro Pro Thr Ala
166 450 455 460
167 Pro Ser Pro Phe Leu Phe Ser Glu Thr Thr Ala Met Lys Cys Arg Ser
168 465 470 475 480
169 Pro Gly Cys Pro Phe Thr Leu Asn Val Gln His Asn Gly Phe Cys Glu
170 485 490 495
171 Arg Cys His Asn Ala Arg Gln Leu His Ala Ser His Ala Pro Asp His
172 500 505 510
173 Thr Arg His Leu Asp Pro Gly Lys Cys Gln Ala Cys Leu Gln Asp Val
174 515 520 525
175 Thr Arg Thr Phe Asn Gly Ile Cys Ser Thr Cys Phe Lys Arg Thr Thr
176 530 535 540
177 Ala Glu Ala Ser Ser Ser Leu Ser Thr Ser Leu Pro Pro Ser Cys His
178 545 550 555 560
179 Gln Arg Ser Lys Ser Asp Pro Ser Arg Leu Val Arg Ser Pro Ser Pro
180 565 570 575
181 His Ser Cys His Arg Ala Gly Asn Asp Ala Pro Ala Gly Cys Leu Ser
182 580 585 590
183 Gln Ala Ala Arg Thr Pro Gly Asp Arg Thr Gly Thr Ser Lys Cys Arg
184 595 600 605
185 Lys Ala Gly Cys Val Tyr Phe Gly Thr Pro Glu Asn Lys Gly Phe Cys
186 610 615 620
187 Thr Leu Cys Phe Ile Glu Tyr Arg Glu Asn Lys His Phe Ala Ala Ala
188 625 630 635 640
189 Ser Gly Lys Val Ser Pro Thr Ala Ser Arg Phe Gln Asn Thr Ile Pro
190 645 650 655
191 Cys Leu Gly Arg Glu Cys Gly Thr Leu Gly Ser Thr Met Phe Glu Gly
192 660 665 670
193 Tyr Cys Gln Lys Cys Phe Ile Glu Ala Gln Asn Gln Arg Phe His Glu
194 675 680 685
195 Ala Lys Arg Thr Glu Glu Gln Leu Arg Ser Ser Gln Arg Arg Asp Val
196 690 695 700
197 Pro Arg Thr Thr Gln Ser Thr Ser Arg Pro Lys Cys Ala Arg Ala Ser
198 705 710 715 720
199 Cys Lys Asn Ile Leu Ala Cys Arg Ser Glu Glu Leu Cys Met Glu Cys
200 725 730 735
201 Gln His Pro Asn Gln Arg Met Gly Pro Gly Ala His Arg Gly Glu Pro
202 740 745 750
203 Ala Pro Glu Asp Pro Pro Lys Gln Arg Cys Arg Ala Pro Ala Cys Asp
204 755 760 765
205 His Phe Gly Asn Ala Lys Cys Asn Gly Tyr Cys Asn Glu Cys Phe Gln

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208 785      790
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212 <211> LENGTH: 1224
213 <212> TYPE: DNA
214 <213> ORGANISM: Human
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: 36, 91, 645, 655, 660, 671, 672
219 <223> OTHER INFORMATION: n = A,T,C or G
221 <221> NAME/KEY: allele
222 <222> LOCATION: (0)...(0)
224 <400> SEQUENCE: 3
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227 gctccttgcc agctcttctt ctcctctcac agccgccaga cccgcctgct gagcccccat 180
228 ggcccgcgct gctctctccg ccgccccag caatccccgg ctcctgcgag tggcgctgct 240
229 gctcctgctc ctggtagccg ctggccggcg cgcagcagga ggcgccctgg ccactgaact 300
230 gcgctgccag tgcttgca gaacctgcagg aattcacctc aagaacatcc aaagtgtgaa 360
231 ggtgaagtcc cccggacccc actgcgcccc aaccgaagtc atagccacac tcaagaatgg 420
232 gcagaaagct tgtctcaacc ccgcatcgcc catggttaag aaaatcatcg aaaagatgct 480
233 gaaaaatggc aaatccaact gaccagaagg aaggaggaag cttattggtg gctgttcctg 540
234 aaggaggccc tgcccttaca ggaacagaag aggaaagaga gacacagctg cagaggccac 600
W--> 235 ctgggattgc gcctaattgtg tttgagcatc acttaggaga aggcncgat taatnaattn 660
W--> 236 attaatttat nnattggttg gttttagaag attctatggt aatattttat gtgtaaaata 720
237 aggttatgat tgaatctact tgcacactct cccattatat ttattgttta ttttaggtca 780
238 aacccaagtt agttcaatcc tgattcatat ttaatttgaa gatagaaggt ttgcagatat 840
239 tctctagtca tttgttaata tttcttcgtg atgacatata acatgtcagc cactgtgata 900
240 gaggtgagg aatccaagaa aatggccagt aagatcaatg tgacggcagg gaaatgtatg 960
241 tgtgtctatt ttgtaactgt aaagatgaat gtcagttgtt atttattgaa atgatttcac 1020
242 agtgtgtggt caacatttct catgttgaag cttaagaac taaaatgttc taaatatccc 1080
243 ttggacattt tatgtctttc ttgtaaggca tactgccttg ttaaatgtta attatgcagt 1140
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248 <211> LENGTH: 107
249 <212> TYPE: PRT
250 <213> ORGANISM: Human
252 <400> SEQUENCE: 4
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256      20      25      30
257 Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
258      35      40      45
259 Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser
260      50      55      60
261 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn

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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/003,608

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11